

SEQUENCE LISTING

<110> McCance, Dennis
Westbrook, III, Thomas F.

<120> E7 REGULATION OF P21 (CIP1) THROUGH AKT

<130> 21108.0016U2

<140> 10/511,814

<141> Unassigned

<150> PCT/US03/12667

<151> 2003-04-21

<150> 60/374,245

<151> 2002-04-19

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 1

Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser
1				5					10					15	
His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu
			20					25				30			
Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro
			35				40					45			
Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg
			50			55				60					
Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg
65				70					75					80	
Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met
			85						90					95	
Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn
			100					105					110		
Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg
			115				120					125			
Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu
			130			135					140				
Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys
145					150					155				160	
Met	Lys	Ala	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	
			165					170					175		
Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu
			180					185					190		
Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg
			195				200						205		

```

Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala
 210                215                220
Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met
225                230                235                240
Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln
                245                250                255
Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr
                260                265                270
Gln

```

```

<210> 2
<211> 344
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct

```

```

<400> 2
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
 1                5                10                15
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
                20                25                30
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
 35                40                45
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
 50                55                60
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
 65                70                75                80
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
                85                90                95
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
                100                105                110
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
                115                120                125
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
                130                135                140
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
 145                150                155                160
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
                165                170                175
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
                180                185                190
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
                195                200                205
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
                210                215                220
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
 225                230                235                240
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
                245                250                255
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
                260                265                270
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
                275                280                285
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
                290                295                300
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
 305                310                315                320

```

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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
```

```
<210> 4
<211> 164
<212> PRT
<213> Artificial Sequence
```

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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
```

[illegible]

```
<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
```

<400> 5

Ala	Thr	Gly	Thr	Cys	Ala	Gly	Ala	Ala	Cys	Cys	Gly	Gly	Cys	Thr	Gly	1	5	10	15
Gly	Gly	Gly	Ala	Thr	Gly	Thr	Cys	Cys	Gly	Thr	Cys	Ala	Gly	Ala	Ala	20	25	30	
Cys	Cys	Cys	Ala	Thr	Gly	Cys	Gly	Gly	Cys	Ala	Gly	Cys	Ala	Ala	Gly	35	40	45	
Gly	Cys	Cys	Thr	Gly	Cys	Cys	Gly	Cys	Cys	Gly	Cys	Cys	Thr	Cys	Thr	50	55	60	
Thr	Cys	Gly	Gly	Cys	Cys	Ala	Gly	Thr	Gly	Gly	Ala	Cys	Ala	Gly		65	70	75	80
Cys	Gly	Ala	Gly	Cys	Ala	Gly	Cys	Thr	Gly	Ala	Gly	Cys	Cys	Gly	Cys	85	90	95	
Gly	Ala	Cys	Thr	Gly	Thr	Gly	Ala	Thr	Gly	Cys	Gly	Cys	Thr	Ala	Ala	100	105	110	
Thr	Gly	Gly	Cys	Gly	Gly	Gly	Cys	Thr	Gly	Cys	Ala	Thr	Cys	Cys	Ala	115	120	125	
Gly	Gly	Ala	Gly	Gly	Cys	Cys	Gly	Thr	Gly	Ala	Gly	Cys	Gly	Ala		130	135	140	
Thr	Gly	Gly	Ala	Ala	Cys	Thr	Thr	Cys	Gly	Ala	Cys	Thr	Thr	Thr	Gly	145	150	155	160
Thr	Cys	Ala	Cys	Cys	Gly	Ala	Gly	Ala	Cys	Ala	Cys	Cys	Ala	Cys	Thr	165	170	175	
Gly	Gly	Ala	Gly	Gly	Gly	Thr	Gly	Ala	Cys	Thr	Thr	Cys	Gly	Cys	Cys	180	185	190	
Thr	Gly	Gly	Gly	Ala	Gly	Cys	Gly	Thr	Gly	Thr	Gly	Cys	Gly	Gly	Gly	195	200	205	
Gly	Cys	Cys	Thr	Thr	Gly	Gly	Cys	Cys	Thr	Gly	Cys	Cys	Cys	Ala	Ala	210	215	220	
Gly	Cys	Thr	Cys	Thr	Ala	Cys	Cys	Thr	Thr	Cys	Cys	Cys	Ala	Cys	Gly	225	230	235	240
Gly	Gly	Gly	Cys	Cys	Cys	Cys	Gly	Gly	Cys	Gly	Ala	Gly	Gly	Cys	Cys	245	250	255	
Gly	Gly	Gly	Ala	Thr	Gly	Ala	Gly	Thr	Thr	Gly	Gly	Gly	Ala	Gly	Gly	260	265	270	
Ala	Gly	Gly	Cys	Ala	Gly	Gly	Cys	Gly	Gly	Cys	Cys	Thr	Gly	Gly	Cys	275	280	285	
Ala	Cys	Cys	Thr	Cys	Ala	Cys	Cys	Thr	Gly	Cys	Thr	Cys	Thr	Gly	Cys	290	295	300	
Thr	Gly	Cys	Ala	Gly	Gly	Gly	Gly	Ala	Cys	Ala	Gly	Cys	Ala	Gly	Ala	305	310	315	320
Gly	Gly	Ala	Ala	Gly	Ala	Cys	Cys	Ala	Thr	Gly	Thr	Gly	Gly	Ala	Cys	325	330	335	
Cys	Thr	Gly	Thr	Cys	Ala	Cys	Thr	Gly	Thr	Cys	Thr	Thr	Gly	Thr	Ala	340	345	350	
Cys	Cys	Cys	Thr	Thr	Gly	Thr	Gly	Cys	Cys	Thr	Cys	Gly	Cys	Thr	Cys	355	360	365	
Ala	Gly	Gly	Gly	Gly	Ala	Gly	Cys	Ala	Gly	Gly	Cys	Thr	Gly	Ala	Ala	370	375	380	
Gly	Gly	Gly	Thr	Cys	Cys	Cys	Cys	Ala	Gly	Gly	Thr	Gly	Gly	Ala	Cys	385	390	395	400
Cys	Thr	Gly	Gly	Ala	Gly	Ala	Cys	Thr	Cys	Thr	Cys	Ala	Gly	Gly	Gly	405	410	415	
Thr	Cys	Gly	Ala	Ala	Ala	Ala	Cys	Gly	Gly	Cys	Gly	Gly	Cys	Ala	Gly	420	425	430	
Ala	Cys	Cys	Ala	Gly	Cys	Ala	Thr	Gly	Ala	Cys	Ala	Gly	Ala	Thr	Thr	435	440	445	
Thr	Cys	Thr	Ala	Cys	Cys	Ala	Cys	Thr	Cys	Cys	Ala	Ala	Ala	Cys	Gly	450	455	460	

Cys Cys Gly Gly Cys Thr Gly Ala Thr Cys Thr Thr Cys Thr Cys Cys
 465 470 475 480
 Ala Ala Gly Ala Gly Gly Ala Ala Gly Cys Cys Cys Thr Ala Ala
 485 490 495

<210> 6
 <211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 6
 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
 1 5 10 15
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
 20 25 30
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
 35 40 45
 Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
 50 55 60
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
 65 70 75 80
 Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
 85 90 95
 Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
 100 105 110
 Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
 115 120 125
 Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
 130 135 140
 Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
 145 150 155 160
 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
 165 170 175
 Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
 180 185 190
 Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
 195 200 205
 Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
 210 215 220
 Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
 225 230 235 240
 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
 245 250 255
 Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr
 260 265 270
 Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile
 275 280 285
 Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala
 290 295 300
 Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val
 305 310 315 320
 Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly
 325 330 335
 Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln
 340 345 350
 Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe
 355 360 365

```

Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu
  370                               375                               380
Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys
385                               390                               395                               400
Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val
                               405                               410                               415
Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu
                               420                               425                               430
Thr Asp Thr Arg Tyr Phe Asp Glu Phe Thr Ala Gln Met Ile Thr
                               435                               440                               445
Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu
                               450                               455                               460
Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala
465                               470                               475                               480

```

<210> 7

<211> 1443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 7

```

atgagcgacg tggctattgt gaaggagggt tggctgcaca aacgagggga gtacatcaag      60
acctggcggc cacgctactt cctcctcaag aatgatggca ccttcattgg ctacaaggag      120
cggccgcagg atgtggacca acgtgaggct cccctcaaca acttctctgt ggcgcagtgc      180
cagctgatga agacggagcg gccccggccc aacacettca tcatccgctg cctgcagtgg      240
accactgtca tcgaacgcac cttccatgtg gagactcctg aggagcggga ggagtggaca      300
accgccatcc agactgtggc tgacggcctc aagaagcagg aggaggagga gatggacttc      360
cggtcgggct caccagtgga caactcaggg gctgaagaga tggagggtgtc cctggccaag      420
ccaagcacc gcgtgaccat gaacgagttt gactacctga agctgctggg caagggcact      480
ttcggcaagg tgatcctggt gaaggagaag gccacaggcc gctactacgc catgaagatc      540
ctcaagaagg aagtcatcgt ggccaaggac gaggtggccc acacactcac cgagaaccgc      600
gtcctgcaga actccaggca ccccttcttc acagccctga agtactcttt ccagaccac      660
gacgcctct gctttgtcat ggagtacgcc aacgggggcg agctgttctt ccacctgtcc      720
cggaacgtg tgttctccga ggaccgggcc cgcttctatg gcgctgagat tgtgtcagcc      780
ctggactacc tgcactcggg gaagaacgtg gtgtaccggg acctcaagct ggagaacctc      840
atgctggaca aggacgggca cattaagatc acagacttcg ggctgtgcaa ggaggggatc      900
aaggacggtg ccaccatgaa gaccttttgc ggcacacctg agtacctggc ccccgagggtg      960
ctggaggaca atgactacgg ccgtgcagtg gactggtggg ggctgggctg ggtcatgtac     1020
gagatgatgt gcggtcgctt gcccttctac aaccaggacc atgagaagct ttttgagctc     1080
atcctcatgg aggagatccg cttcccgcgc acgcttggtc ccgaggccaa gtccttgctt     1140
tcagggtctg tcaagaagga cccaagcag aggccttggcg ggggctccga ggacgccaaag     1200
gagatcatgc agcatcgctt ctttgccggt atcgtgtggc agcacgtgta cgagaagaag     1260
ctcagcccac ccttcaagcc ccaggtcacg tcggagactg acaccaggta ttttgatgag     1320
gagttcacgg ccagatgat caccatcaca ccacctgacc aagatgacag catggagtgt     1380
gtggacagcg agcgcaggcc ccacttcccc cagtttctct actcggccag cagcacggcc     1440
tga                                                                 1443

```

<210> 8

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 8

```

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
 1           5           10           15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
           20           25           30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
           35           40           45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
           50           55           60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65           70           75           80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
           85           90           95
Lys Pro

```

<210> 9

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 9

```

atgcatggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgcccatct gttctcagaa acca          294

```

<210> 10

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 10

```

atgcacggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgcccatct gttctcagaa acca          294

```

<210> 11

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 11

```

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
 1           5           10           15

```

```

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
      20      25      30
Glu Glu Glu Asp Glu Val Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
      35      40      45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
      50      55      60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65      70      75      80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
      85      90      95
Lys Pro

```

<210> 12
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

```

<400> 12
atgcatggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca          294

```

<210> 13
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

```

<400> 13
atgcacggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca          294

```

<210> 14
 <211> 648
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

```

<400> 14
Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
  1      5      10      15
Leu Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
      20      25      30
Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
      35      40      45

```


Thr	Asp	Ser	Ser	Lys	Thr	Ser	Asn	Thr	Ile	Arg	Val	Phe	Leu	Pro	Asn
50						55					60				
Lys	Gln	Arg	Thr	Val	Val	Asn	Val	Arg	Asn	Gly	Met	Ser	Leu	His	Asp
65				70						75					80
Cys	Leu	Met	Lys	Ala	Leu	Lys	Val	Arg	Gly	Leu	Gln	Pro	Glu	Cys	Cys
				85					90					95	
Ala	Val	Phe	Arg	Leu	Leu	Gln	Glu	His	Lys	Gly	Lys	Lys	Ala	Arg	Leu
			100					105					110		
Asp	Trp	Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Glu	Glu	Leu	Gln	Val
		115					120					125			
Asp	Phe	Leu	Asp	His	Val	Pro	Leu	Thr	Thr	His	Asn	Phe	Ala	Arg	Lys
	130					135					140				
Thr	Phe	Leu	Lys	Leu	Ala	Phe	Cys	Asp	Ile	Cys	Gln	Lys	Phe	Leu	Leu
145				150						155					160
Asn	Gly	Phe	Arg	Cys	Gln	Thr	Cys	Gly	Tyr	Lys	Phe	His	Glu	His	Cys
				165				170						175	
Ser	Thr	Lys	Val	Pro	Thr	Met	Cys	Val	Asp	Trp	Ser	Asn	Ile	Arg	Gln
			180					185					190		
Leu	Leu	Leu	Phe	Pro	Asn	Ser	Thr	Ala	Ser	Asp	Ser	Gly	Val	Pro	Ala
		195					200					205			
Pro	Pro	Ser	Phe	Thr	Met	Arg	Arg	Met	Arg	Glu	Ser	Val	Ser	Arg	Met
	210					215					220				
Pro	Ala	Ser	Ser	Gln	His	Arg	Tyr	Ser	Thr	Pro	His	Ala	Phe	Thr	Phe
225				230						235					240
Asn	Thr	Ser	Ser	Pro	Ser	Ser	Glu	Gly	Ser	Leu	Ser	Gln	Arg	Gln	Arg
				245				250						255	
Ser	Thr	Ser	Thr	Pro	Asn	Val	His	Met	Val	Ser	Thr	Thr	Leu	Pro	Val
			260					265					270		
Asp	Ser	Arg	Met	Ile	Glu	Asp	Ala	Ile	Arg	Ser	His	Ser	Glu	Ser	Ala
	275						280					285			
Ser	Pro	Ser	Ala	Leu	Ser	Ser	Ser	Pro	Asn	Asn	Leu	Ser	Pro	Thr	Gly
	290					295					300				
Trp	Ser	Gln	Pro	Lys	Thr	Pro	Val	Pro	Ala	Gln	Arg	Glu	Arg	Ala	Pro
305				310						315					320
Gly	Ser	Gly	Thr	Gln	Glu	Lys	Asn	Lys	Ile	Arg	Pro	Arg	Gly	Gln	Arg
				325					330					335	
Asp	Ser	Ser	Tyr	Trp	Glu	Ile	Glu	Ala	Ser	Glu	Val	Met	Leu	Ser	
			340				345					350			
Thr	Arg	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Lys	Trp
		355					360					365			
His	Gly	Asp	Val	Ala	Val	Lys	Ile	Leu	Lys	Val	Val	Asp	Pro	Thr	Pro
	370					375					380				
Glu	Gln	Leu	Gln	Ala	Phe	Arg	Asn	Glu	Val	Ala	Val	Leu	Arg	Lys	Thr
385				390						395					400
Arg	His	Val	Asn	Ile	Leu	Leu	Phe	Met	Gly	Tyr	Met	Thr	Lys	Asp	Asn
			405						410					415	
Leu	Ala	Ile	Val	Thr	Gln	Trp	Cys	Glu	Gly	Ser	Ser	Leu	Tyr	Lys	His
			420					425					430		
Leu	His	Val	Gln	Glu	Thr	Lys	Phe	Gln	Met	Phe	Gln	Leu	Ile	Asp	Ile
		435					440					445			
Ala	Arg	Gln	Thr	Ala	Gln	Gly	Met	Asp	Tyr	Leu	His	Ala	Lys	Asn	Ile
	450					455					460				
Ile	His	Arg	Asp	Met	Lys	Ser	Asn	Asn	Ile	Phe	Leu	His	Glu	Gly	Leu
465				470						475					480
Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala	Thr	Val	Lys	Ser	Arg	Trp
				485					490					495	
Ser	Gly	Ser	Gln	Gln	Val	Glu	Gln	Pro	Thr	Gly	Ser	Val	Leu	Trp	Met
			500					505					510		
Ala	Pro	Glu	Val	Ile	Arg	Met	Gln	Asp	Asn	Asn	Pro	Phe	Ser	Phe	Gln
		515					520					525			

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Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
  530                               535                               540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545                               550                               555                               560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Arg Leu Tyr Lys Asn
                               565                               570                               575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
                               580                               585                               590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
                               595                               600                               605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
                               610                               615                               620
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625                               630                               635                               640
Thr Ser Pro Arg Leu Pro Val Phe
                               645

```

<210> 15

<211> 2977

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 15

```

ccgaatgtga ccgcctcccc ctccctcacc cgccgcgggg aggaggagcg ggcgagaagc      60
tgcgcgcgaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa      120
gctgcatcaa tggagcacat acaggagact tggagacga tcagcaatgg ttttggattc      180
aaagatgccg tgtttgatgg ctccagctgc atctctccta caatagttca gcagtttggc      240
tatcagcgcc gggcatcaga tgatggcaaa ctcacagatc cttctaagac aagcaacact      300
atccgtgttt tcttgccgaa caagcaaaga acagtgggtc atgtgcgaaa tggaatgagc      360
ttgcatgact gccttatgaa agcactcaag gtgagggggc tgcaaccaga gtgctgtgca      420
gtgttcagac ttctccacga acacaaaggt aaaaaagcac gcttagattg gaatactgat      480
gctgcgtctt tgattggaga agaacttcaa gtagatttcc tggatcatgt tcccctcaca      540
acacacaact ttgctcgga gacgttcctg aagcttgctt tctgtgacat ctgtcagaaa      600
ttctgtctca atggatttcg atgtcagact tgtggctaca aatttcatga gcactgtagc      660
accaaagtac ctactatgtg tgtggactgg agtaacatca gacaactctt attgtttcca      720
aattccacta ttggtgatag tggagtccca gcactacctt ctttgactat gcgtcgtatg      780
cgagagtctg tttccaggat gcctgttagt tctcagcaca gatattctac acctcacgcc      840
ttcaccttta acacctccag tccctcatct gaagggtccc tctcccagag gcagaggctc      900
acatccacac ctaatgtcca catggtcagc accacgctgc ctgtggacag caggatgatt      960
gaggatgcaa ttcgaagtca cagcgaatca gcctcacctt cagecctgtc cagtagcccc     1020
aacaatctga gcccaacagg ctggtcacag ccgaaaaccc ccgtgccagc acaaagagag     1080
cgggcaccag tatctgggac ccaggagaaa aacaaaatta ggcctcgtgg acagagagat     1140
tcaagctatt attgggaaat agaagccagt gaagtgatgc tgtccactcg gattgggtca     1200
ggctcttttg gaactgttta taagggtaaa tggcacggag atgttgacgt aaagatccta     1260
aaggttgtcg acccaacccc agagcaattc caggccttca ggaatgaggt ggctgttctg     1320
cgcaaaacac ggcattgtgaa cattctgctt ttcattgggt acatgacaaa ggacaacctg     1380
gcaattgtga ccagtggtg cgagggcagc agcctctaca aacacctgca tgtccaggag     1440
accaagtttc agatgttcca gctaattgac attgcccggc agacggctca gggaatggac     1500
tatttgcatt caaagaacat catccataga gacatgaaa ccaacaatat atttctccat     1560
gaaggcttaa cagtgaataa tggagatttt ggtttggcaa cagtaaagtc acgctggagt     1620
ggttctcagc aggttgaaca acctactggc tctgtcctct ggatggcccc agaggtgatc     1680
cgaatgcagg ataacaaccc attcagtttc cagtcggatg tctactccta tggcatcgta     1740
ttgtatgaac tgatgacggg ggagcttcct tattctcaca tcaacaaccg agatcagatc     1800
atcttcatgg tgggcccagg atatgcctcc ccagatctta gtaagctata taagaactgc     1860
cccaaagcaa tgaagaggct ggtagctgac tgtgtgaaga aagtaaagga agagaggcct     1920
ctttttcccc agatcctgtc ttccattgag ctgctccaac actctctacc gaagatcaac     1980
cggagcgctt ccgagccatc cttgcatcgg gcagcccaca ctgaggatat caatgcttgc     2040

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```

acgctgacca cgtccccgag gctgcctgtc ttctagttga ctttgcacct gtcttcaggc 2100
tgccagggga ggaggagaag ccagcaggca ccacttttct gctccctttc tccagaggca 2160
gaacacatgt tttcagagaa gctctgctaa ggaccttcta gactgctcac agggccttaa 2220
cttcatgttg ctttcttttc tatccctttg ggccctggga gaaggaagcc atttgcagtg 2280
ctggtgtgtc ctgctccctc cccacattcc ccattgctcaa ggcccagcct tctgtagatg 2340
cgcaagtgga tgttgatggg agtacaaaaa gcagggggccc agccccagct gttgggtaca 2400
tgagtattta gaggaagtaa ggtagcaggc agtccagccc tgatgtggag acacatggga 2460
ttttggaaat cagcttcttg aggaatgcat gtcacaggcg ggactttctt cagagagtgg 2520
tgcagcgcca gacattttgc acataaggca ccaaacagcc caggactgcc gagactctgg 2580
ccgcccgaag gagcctgctt tggactatg gaacttttct taggggacac gtccctcttt 2640
cacagcttct aagggtgtcca gtgcattggg atgggtttcc aggcaaggca ctcgccaat 2700
ccgcatctca gccctctcag gagcagtctt ccattcatgct gaattttgtc ttccaggagc 2760
tgccctatg gggcgggccg cagggccagc ctgtttctct aacaaacaaa caaacaacaa 2820
gccttgtttc tctagtcaca tcatgtgtat acaaggaagc caggaataca ggttttcttg 2880
atgatttggg ttttaatttt gtttttattg cacctgacaa aatacagtta tctgatggtc 2940
cctcaattat gttattttta taaaataaat taaatttt 2977

```

<210> 16

<211> 813

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 16

```

Met Ser Arg Ile Asn Phe Lys Lys Ser Ser Ala Ser Thr Thr Pro Thr
1           5           10           15
Ser Pro His Cys Pro Ser Pro Arg Leu Ile Ser Leu Pro Arg Cys Ala
20           25           30
Ser Ser Ser Ile Asp Arg Lys Asp Gln Ala Ser Pro Met Ala Ser Pro
35           40           45
Ser Thr Pro Leu Tyr Pro Lys His Ser Asp Ser Leu His Ser Leu Ser
50           55           60
Gly His His Ser Ala Gly Gly Ala Gly Thr Ser Asp Lys Glu Pro Pro
65           70           75           80
Lys Phe Lys Tyr Lys Met Ile Met Val His Leu Pro Phe Asp Gln His
85           90           95
Ser Arg Val Glu Val Arg Pro Gly Glu Thr Ala Arg Asp Ala Ile Ser
100          105          110
Lys Leu Leu Lys Lys Arg Asn Ile Thr Pro Gln Leu Cys His Val Asn
115          120          125
Ala Ser Ser Asp Pro Lys Gln Glu Ser Ile Glu Leu Ser Leu Thr Met
130          135          140
Glu Glu Ile Ala Ser Arg Leu Pro Gly Asn Glu Leu Trp Val His Ser
145          150          155          160
Glu Tyr Leu Asn Thr Val Ser Ser Ile Lys His Ala Ile Val Arg Arg
165          170          175
Thr Phe Ile Pro Pro Lys Ser Cys Asp Val Cys Asn Asn Pro Ile Trp
180          185          190
Met Met Gly Phe Arg Cys Glu Phe Cys Gln Phe Lys Phe His Gln Arg
195          200          205
Cys Ser Ser Phe Ala Pro Leu Tyr Cys Asp Leu Leu Gln Ser Val Pro
210          215          220
Lys Asn Glu Asp Leu Val Lys Glu Leu Phe Gly Ile Ala Ser Gln Val
225          230          235          240
Glu Gly Pro Asp Arg Ser Val Ala Glu Ile Val Leu Ala Asn Leu Ala
245          250          255
Pro Thr Ser Gly Gln Ser Pro Ala Ala Thr Pro Asp Ser Ser His Pro
260          265          270

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Asp	Leu	Thr	Ser	Ile	Lys	Arg	Thr	Gly	Gly	Val	Lys	Arg	His	Pro	Met	275	280	285
Ala	Val	Ser	Pro	Gln	Asn	Glu	Thr	Ser	Gln	Leu	Ser	Pro	Ser	Gly	Pro	290	295	300
Tyr	Pro	Arg	Asp	Arg	Ser	Ser	Ser	Ala	Pro	Asn	Ile	Asn	Ala	Ile	Asn	305	310	315
Asp	Glu	Ala	Thr	Val	Gln	His	Asn	Gln	Arg	Ile	Leu	Asp	Ala	Leu	Glu	325	330	335
Ala	Gln	Arg	Leu	Glu	Glu	Glu	Ser	Arg	Asp	Lys	Thr	Gly	Ser	Leu	Leu	340	345	350
Ser	Thr	Gln	Ala	Arg	His	Arg	Pro	His	Phe	Gln	Ser	Gly	His	Ile	Leu	355	360	365
Ser	Gly	Ala	Arg	Met	Asn	Arg	Leu	His	Pro	Leu	Val	Asp	Cys	Thr	Pro	370	375	380
Leu	Gly	Ser	Asn	Ser	Pro	Ser	Ser	Thr	Cys	Ser	Ser	Pro	Pro	Gly	Gly	385	390	395
Leu	Ile	Gly	Gln	Pro	Thr	Leu	Gly	Gln	Ser	Pro	Asn	Val	Ser	Gly	Ser	405	410	415
Thr	Thr	Ser	Ser	Leu	Val	Ala	Ala	His	Leu	His	Thr	Leu	Pro	Leu	Thr	420	425	430
Pro	Pro	Gln	Ser	Ala	Pro	Pro	Gln	Lys	Ile	Ser	Pro	Gly	Phe	Phe	Arg	435	440	445
Asn	Arg	Ser	Arg	Ser	Pro	Gly	Glu	Arg	Leu	Asp	Ala	Gln	Arg	Pro	Arg	450	455	460
Pro	Pro	Gln	Lys	Pro	His	His	Glu	Asp	Trp	Glu	Ile	Leu	Pro	Asn	Glu	465	470	475
Phe	Ile	Ile	Gln	Tyr	Lys	Val	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	485	490	495
Arg	Gly	Glu	Phe	Gly	Thr	Val	Ala	Ile	Lys	Lys	Leu	Asn	Val	Val		500	505	510
Asp	Pro	Thr	Pro	Ser	Gln	Met	Ala	Ala	Phe	Lys	Asn	Glu	Val	Ala	Val	515	520	525
Leu	Lys	Lys	Thr	Arg	His	Leu	Asn	Val	Leu	Leu	Phe	Met	Gly	Trp	Val	530	535	540
Arg	Glu	Pro	Glu	Ile	Ala	Ile	Ile	Thr	Gln	Trp	Cys	Glu	Gly	Ser	Ser	545	550	555
Leu	Tyr	Arg	His	Ile	His	Val	Gln	Glu	Pro	Arg	Val	Glu	Phe	Glu	Met	565	570	575
Gly	Ala	Ile	Ile	Asp	Ile	Leu	Lys	Gln	Val	Ser	Leu	Gly	Met	Asn	Tyr	580	585	590
Leu	His	Ser	Lys	Asn	Ile	Ile	His	Arg	Asp	Leu	Lys	Thr	Asn	Asn	Ile	595	600	605
Phe	Leu	Met	Asp	Asp	Met	Ser	Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	610	615	620
Ala	Thr	Val	Lys	Thr	Lys	Trp	Thr	Val	Asn	Gly	Gly	Gln	Gln	Gln	Gln	625	630	635
Gln	Pro	Thr	Gly	Ser	Ile	Leu	Trp	Met	Ala	Pro	Glu	Val	Ile	Arg	Met	645	650	655
Gln	Asp	Asp	Asn	Pro	Tyr	Thr	Pro	Gln	Ser	Asp	Val	Tyr	Ser	Phe	Gly	660	665	670
Ile	Cys	Met	Tyr	Glu	Ile	Leu	Ser	Ser	His	Leu	Pro	Tyr	Ser	Asn	Ile	675	680	685
Asn	Asn	Arg	Asp	Gln	Ile	Leu	Phe	Met	Val	Gly	Arg	Gly	Tyr	Leu	Arg	690	695	700
Pro	Asp	Arg	Ser	Lys	Ile	Arg	His	Asp	Thr	Pro	Lys	Ser	Met	Leu	Lys	705	710	715
Leu	Tyr	Asp	Asn	Cys	Ile	Met	Phe	Asp	Arg	Asn	Glu	Arg	Pro	Val	Phe	725	730	735
Gly	Glu	Val	Leu	Glu	Arg	Leu	Arg	Asp	Ile	Ile	Leu	Pro	Lys	Leu	Thr	740	745	750

Arg Ser Gln Ser Ala Pro Asn Val Leu His Leu Asp Ser Gln Tyr Ser
 755 760 765
 Val Met Asp Ala Val Met Arg Ser Gln Met Leu Ser Trp Ser Tyr Ile
 770 775 780
 Pro Pro Ala Thr Ala Lys Thr Pro Gln Ser Ala Ala Ala Ala Ala Ala
 785 790 795 800
 Arg Asn Lys Lys Ala Tyr Tyr Asn Val Tyr Gly Leu Ile
 805 810

<210> 17
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 17
 atggagagag acttcgacct tggcatgggc agacctggcg ggctcggagg acttggtggt 60
 gaaccgatca tgcaacaaat gccacagcca gcgcctcatc atccatcccg tagtagtaac 120
 gaccacaatg tgaagaacct catgaagcag gccgaggaga actccggata tctcacattg 180
 caaggttaacc gtcgtaaagc tgacttgaag gagcttcagt tcgtggaaga tattggtcat 240
 ggaagctgcg gtacgggtcac aaagtgcaga tacaagagtg tgatcatggc tgtgaagacg 300
 atgcctcggg cgtcaaacag ttatgaaatg tcccgcattt tgatggatct tgacgtcatc 360
 tgtctctctt tcgactgtcc gtacattgta cgttgcttcg gatacttcat caccaacttc 420
 gacgtccgtg tctgcatgga gtgcatggct acttgccctg accgtctgct tatccgcac 480
 aagcagccaa ttccagagag aattattgga aagttgagtg tgagcatcat taaagctctg 540
 cactacttga aaaccaagca ccaaatcatg caccgtgatg tgaagccatc aaacattctc 600
 ctcgactgga gtggcggtcat caagctttgc gatttcggta ttgctggcag actgatcgag 660
 tctcgtgctc attcgaagca agccggatgc cctctgtaca tgggtcctga gcgcctcgac 720
 cccaacaact ttgactcgta tgacattcgc agtgacgtgt ggtcttttgg tgttactttg 780
 gtcgagctgg caaccggaca gtaccatac gccggaaccg aattcgacat gatgtccaag 840
 attctcaatg acgagccacc gcgcctggat ccggccaaat tctctccgga cttctgtcaa 900
 ctcgtcgaga gctgcctgca gcgtgatcca acgatgcgtc ccaattacga tatgctcctc 960
 cagcatccgt ttgtcgtgca tcacgagaaa attgaaaccg acgtcgagga gtggtttg 1020
 gatgtgatgg gcgagtgcgg ataa 1044

<210> 18
 <211> 1493
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 18
 Met Ala Ala Ala Ala Gly Asp Arg Ala Ser Ser Ser Gly Phe Pro Gly
 1 5 10 15
 Ala Ala Ala Ala Ser Pro Glu Ala Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Ala Leu Gln Gly Ser Gly Ala Pro Ala Ala Gly Ala Ala Gly Leu Leu
 35 40 45
 Arg Glu Pro Gly Ser Ala Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg
 50 55 60
 Gln Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln
 65 70 75 80
 Pro Leu Phe Leu Ala Ala Ala Ser Pro Pro Cys Pro Ser Thr Ser Pro
 85 90 95

Ser Pro Glu Pro Ala Asp Ala Ala Ala Gly Ala Ser Arg Phe Gln Pro
 100 105 110
 Ala Ala Gly Pro Pro Pro Pro Gly Ala Ala Ser Arg Cys Gly Ser His
 115 120 125
 Ser Ala Glu Leu Ala Ala Ala Arg Asp Ser Gly Ala Arg Ser Pro Ala
 130 135 140
 Gly Ala Glu Pro Pro Ser Ala Ala Ala Pro Ser Gly Arg Glu Met Glu
 145 150 155 160
 Asn Lys Glu Thr Leu Lys Gly Leu His Lys Met Glu Asp Arg Pro Glu
 165 170 175
 Glu Arg Met Ile Arg Glu Lys Leu Lys Ala Thr Cys Met Pro Ala Trp
 180 185 190
 Lys His Glu Trp Leu Glu Arg Arg Asn Arg Arg Gly Pro Val Val Val
 195 200 205
 Lys Pro Ile Pro Ile Lys Gly Asp Gly Ser Glu Val Asn Asn Leu Ala
 210 215 220
 Ala Glu Pro Gln Gly Glu Gly Gln Ala Gly Ser Ala Ala Pro Ala Pro
 225 230 235 240
 Lys Gly Arg Arg Ser Pro Ser Pro Gly Ser Ser Pro Ser Gly Arg Ser
 245 250 255
 Val Lys Pro Glu Ser Pro Gly Val Arg Arg Lys Arg Val Ser Pro Val
 260 265 270
 Pro Phe Gln Ser Gly Arg Ile Thr Pro Pro Arg Arg Ala Pro Ser Pro
 275 280 285
 Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Ser Arg Arg Val Asn
 290 295 300
 Lys Val Met Arg Ala Arg Leu Tyr Leu Leu Gln Ile Gly Pro Asn
 305 310 315 320
 Ser Phe Leu Ile Gly Gly Asp Ser Pro Asp Asn Lys Tyr Arg Val Phe
 325 330 335
 Ile Gly Pro Gln Asn Cys Ser Cys Gly Arg Gly Ala Phe Cys Ile His
 340 345 350
 Leu Leu Phe Val Met Leu Arg Val Phe Gln Leu Glu Pro Ser Asp Pro
 355 360 365
 Met Leu Trp Arg Lys Thr Leu Lys Asn Phe Glu Val Glu Ser Leu Phe
 370 375 380
 Gln Lys Tyr His Ser Arg Arg Ser Ser Arg Ile Lys Ala Pro Ser Arg
 385 390 395 400
 Asn Thr Ile Gln Lys Phe Val Ser Arg Met Ser Asn Ser His Thr Leu
 405 410 415
 Ser Ser Ser Ser Thr Ser Thr Ser Ser Ser Glu Asn Ser Ile Lys Asp
 420 425 430
 Glu Glu Glu Gln Met Cys Pro Ile Cys Leu Leu Gly Met Leu Asp Glu
 435 440 445
 Glu Ser Leu Thr Val Cys Glu Asp Gly Cys Arg Asn Lys Leu His His
 450 455 460
 His Cys Met Ser Ile Trp Ala Glu Glu Cys Arg Arg Asn Arg Glu Pro
 465 470 475 480
 Leu Ile Cys Pro Leu Cys Arg Ser Lys Trp Arg Ser His Asp Phe Tyr
 485 490 495
 Ser His Glu Leu Ser Ser Pro Val Glu Ser Pro Ala Ser Leu Arg Ala
 500 505 510
 Val Gln Gln Pro Ser Ser Pro Gln Gln Pro Val Ala Gly Ser Gln Arg
 515 520 525
 Arg Asn Gln Glu Ser Ser Phe Asn Leu Thr His Phe Gly Thr Gln Gln
 530 535 540
 Ile Pro Ser Ala Tyr Lys Asp Leu Ala Glu Pro Trp Ile Gln Val Phe
 545 550 555 560
 Gly Met Glu Leu Val Gly Cys Leu Phe Ser Arg Asn Trp Asn Val Arg
 565 570 575

Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	Asp	Val	Ser	Gly	Ala	Leu	Leu	580	585	590
Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Gly	595	600	605
Ser	Leu	Ser	Ala	Gly	Ala	Ala	Ser	Gly	Ser	Ser	Gln	Pro	Ser	Ile	Ser	610	615	620
Gly	Asp	Val	Val	Glu	Ala	Cys	Cys	Ser	Val	Leu	Ser	Ile	Val	Cys	Ala	625	630	635
Asp	Pro	Val	Tyr	Lys	Val	Tyr	Val	Ala	Ala	Leu	Lys	Thr	Leu	Arg	Ala	645	650	655
Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	Leu	Ala	Glu	Arg	Ile	Lys	Leu	660	665	670
Gln	Arg	Leu	Leu	Arg	Pro	Val	Val	Asp	Thr	Ile	Leu	Val	Lys	Cys	Ala	675	680	685
Asp	Ala	Asn	Ser	Arg	Thr	Ser	Gln	Leu	Ser	Ile	Ser	Thr	Val	Leu	Glu	690	695	700
Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	Val	Gly	Arg	Glu	Ile	Leu	705	710	715
Lys	Ala	Gly	Ser	Ile	Gly	Val	Gly	Gly	Val	Asp	Tyr	Val	Leu	Ser	Cys	725	730	735
Ile	Leu	Gly	Asn	Gln	Ala	Glu	Ser	Asn	Asn	Trp	Gln	Glu	Leu	Leu	Gly	740	745	750
Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	Glu	Phe	Pro	Ala	Glu	Phe	755	760	765
Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	Gln	Ala	Glu	Pro	Val	Glu	770	775	780
Ile	Arg	Tyr	Lys	Lys	Leu	Ser	Leu	Leu	Thr	Phe	Ala	Leu	Gln	Ser		785	790	795
Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	Leu	Ser	Arg	Arg	Ile	Tyr	805	810	815
Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Ala	Val	Pro	Ala	Val	Phe	Ser	Lys	820	825	830
Leu	Val	Thr	Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	Phe	Thr	Arg	Met	835	840	845
Arg	Arg	Arg	Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	Ile	Ala	Glu	Val	850	855	860
Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His	Gln	Asp	Ser	Leu	865	870	875
Gln	Ala	Val	Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser	Ser	Leu	Glu	His	885	890	895
Thr	Val	His	Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser	Ala	Thr	Arg	Leu	900	905	910
Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Asp	Arg	Leu	Ala	Gly	Val	Ser	Val	915	920	925
Gly	Leu	Pro	Ser	Ser	Thr	Thr	Thr	Glu	Gln	Pro	Lys	Pro	Ala	Val	Gln	930	935	940
Thr	Lys	Gly	Arg	Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	945	950	955
His	Ala	Gln	Leu	Met	Phe	Pro	Ala	Pro	Ser	Ala	Pro	Cys	Ser	Ser	Ala	965	970	975
Pro	Ser	Val	Pro	Asp	Ile	Ser	Lys	His	Arg	Pro	Gln	Ala	Phe	Val	Pro	980	985	990
Cys	Lys	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	Ser	Leu	995	1000	1005
Gln	Phe	Gln	Arg	Asn	Cys	Ser	Glu	His	Arg	Asp	Ser	Asp	Gln	Leu	Ser	1010	1015	1020
Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro	Pro	Pro	Ser	Ser	Asn	Ile	His	Arg	1025	1030	1035
Pro	Lys	Pro	Ser	Arg	Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	1045	1050	1055

Ala Thr Lys Ser Ser Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys
 1060 1065 1070
 Asp Asp Ser Phe Gly Gly Gly Gly Asn Ser Gly Asn Ala Val Ile Pro
 1075 1080 1085
 Ser Asp Glu Thr Val Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp
 1090 1095 1100
 Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser
 1105 1110 1115 1120
 Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val Ala Val
 1125 1130 1135
 Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val
 1140 1145 1150
 Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu
 1155 1160 1165
 Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro
 1170 1175 1180
 Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile
 1185 1190 1195 1200
 Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln
 1205 1210 1215
 Pro Tyr Arg Glu Asp Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu
 1220 1225 1230
 Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr
 1235 1240 1245
 Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu
 1250 1255 1260
 Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly
 1265 1270 1275 1280
 His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu
 1285 1290 1295
 Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val
 1300 1305 1310
 Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile
 1315 1320 1325
 Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn
 1330 1335 1340
 Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser
 1345 1350 1355 1360
 Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu
 1365 1370 1375
 Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly
 1380 1385 1390
 Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly
 1395 1400 1405
 Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala
 1410 1415 1420
 Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His Leu Ala
 1425 1430 1435 1440
 Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser
 1445 1450 1455
 His Leu Ser Pro Gly Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu
 1460 1465 1470
 Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val
 1475 1480 1485
 Phe Arg Thr Thr Trp
 1490

<210> 19

<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 19

Met	Pro	Lys	Lys	Lys	Pro	Thr	Pro	Ile	Gln	Leu	Asn	Pro	Ala	Pro	Asp
1				5					10					15	
Gly	Ser	Ala	Val	Asn	Gly	Thr	Ser	Ser	Ala	Glu	Thr	Asn	Leu	Glu	Ala
			20					25					30		
Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	Gln	Gln	Arg	Lys
		35					40					45			
Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Gln	Lys	Val	Gly	Glu	Leu	Lys
	50					55					60				
Asp	Asp	Asp	Phe	Glu	Lys	Ile	Ser	Glu	Leu	Gly	Ala	Gly	Asn	Gly	Gly
65					70					75					80
Val	Val	Phe	Lys	Val	Ser	His	Lys	Pro	Ser	Gly	Leu	Val	Met	Ala	Arg
				85					90					95	
Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn	Gln	Ile	Ile
			100					105					110		
Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr	Ile	Val	Gly
		115					120					125			
Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	Ile	Cys	Met	Glu
	130					135					140				
His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	Lys	Ala	Gly	Arg
145					150					155					160
Ile	Pro	Glu	Gln	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val	Ile	Lys	Gly
				165					170					175	
Leu	Thr	Tyr	Leu	Arg	Glu	Lys	His	Lys	Ile	Met	His	Arg	Asp	Val	Lys
			180					185					190		
Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys	Leu	Cys	Asp
		195					200					205			
Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn	Ser	Phe	Val
	210					215					220				
Gly	Thr	Arg	Ser	Tyr	Met	Ser	Pro	Glu	Arg	Leu	Gln	Gly	Thr	His	Tyr
225					230					235					240
Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	Leu	Val	Glu	Met
				245					250					255	
Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	Lys	Glu	Leu	Glu
			260				265						270		
Leu	Met	Phe	Gly	Cys	Gln	Val	Glu	Gly	Asp	Ala	Ala	Glu	Thr	Pro	Pro
		275					280					285			
Arg	Pro	Arg	Thr	Pro	Gly	Arg	Pro	Leu	Ser	Ser	Tyr	Gly	Met	Asp	Ser
	290					295					300				
Arg	Pro	Pro	Met	Ala	Ile	Phe	Glu	Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu
305					310					315					320
Pro	Pro	Pro	Lys	Leu	Pro	Ser	Gly	Val	Phe	Ser	Leu	Glu	Phe	Gln	Asp
				325					330					335	
Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu
			340					345					350		
Lys	Gln	Leu	Met	Val	His	Ala	Phe	Ile	Lys	Arg	Ser	Asp	Ala	Glu	Glu
		355					360					365			
Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys	Ser	Thr	Ile	Gly	Leu	Asn	Gln	Pro
	370					375					380				
Ser	Thr	Pro	Thr	His	Ala	Ala	Gly	Val							
385					390										

<210> 20

<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 20

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Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1           5           10           15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
          20           25           30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
          35           40           45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
          50           55           60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65           70           75           80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
          85           90           95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
          100          105          110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
          115          120          125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
          130          135          140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145          150          155          160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
          165          170          175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
          180          185          190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
          195          200          205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
          210          215          220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225          230          235          240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
          245          250          255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
          260          265          270
Leu Leu Phe Gly Cys His Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
          275          280          285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
290          295          300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305          310          315          320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
          325          330          335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
          340          345          350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
          355          360          365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
          370          375          380
Ser Thr Pro Thr His Ala Ala Ser Ile
385          390

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<210> 21

<211> 393

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 21

Met	Pro	Lys	Lys	Lys	Pro	Thr	Pro	Ile	Gln	Leu	Asn	Pro	Ala	Pro	Asp
1				5					10					15	
Gly	Ser	Ala	Val	Asn	Gly	Thr	Ser	Ser	Ala	Glu	Thr	Asn	Leu	Glu	Ala
			20					25					30		
Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	Gln	Gln	Arg	Lys
		35					40					45			
Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Gln	Lys	Val	Gly	Glu	Leu	Lys
	50					55					60				
Asp	Asp	Asp	Phe	Glu	Lys	Ile	Ser	Glu	Leu	Gly	Ala	Gly	Asn	Gly	Gly
65					70					75					80
Val	Val	Phe	Lys	Val	Ser	His	Lys	Pro	Ser	Gly	Leu	Val	Met	Ala	Arg
				85				90						95	
Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn	Gln	Ile	Ile
			100					105					110		
Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr	Ile	Val	Gly
		115					120					125			
Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	Ile	Cys	Met	Glu
	130					135					140				
His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	Lys	Ala	Gly	Arg
145					150					155					160
Ile	Pro	Glu	Gln	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val	Ile	Lys	Gly
				165				170						175	
Leu	Thr	Tyr	Leu	Arg	Glu	Lys	His	Lys	Ile	Met	His	Arg	Asp	Val	Lys
			180					185					190		
Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys	Leu	Cys	Asp
		195				200						205			
Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn	Ser	Phe	Val
	210					215					220				
Gly	Thr	Arg	Ser	Tyr	Met	Ser	Pro	Glu	Arg	Leu	Gln	Gly	Thr	His	Tyr
225					230					235					240
Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	Leu	Val	Glu	Met
				245				250						255	
Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	Lys	Glu	Leu	Glu
			260				265						270		
Leu	Met	Phe	Gly	Cys	Gln	Val	Glu	Gly	Asp	Ala	Ala	Glu	Thr	Pro	Pro
		275				280						285			
Arg	Pro	Arg	Thr	Pro	Gly	Arg	Pro	Leu	Ser	Ser	Tyr	Gly	Met	Asp	Ser
	290				295						300				
Arg	Pro	Pro	Met	Ala	Ile	Phe	Glu	Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu
305					310					315					320
Pro	Pro	Pro	Lys	Leu	Pro	Ser	Gly	Val	Phe	Ser	Leu	Glu	Phe	Gln	Asp
				325				330						335	
Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu
			340				345						350		
Lys	Gln	Leu	Met	Val	His	Ala	Phe	Ile	Lys	Arg	Ser	Asp	Ala	Glu	Glu
	355					360						365			
Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys	Ser	Thr	Ile	Gly	Leu	Asn	Gln	Pro
	370					375					380				
Ser	Thr	Pro	Thr	His	Ala	Ala	Gly	Val							
385					390										